



# SEQUENCE LISTING

<110> He, et al.

<120> Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3 and 4

<130> PF140P1D1

<140> 09/613,508

<141> 2000-07-10

<150> 08/462,969

<151> 1995-06-05

<150> 08/334,251

<151> 1994-11-01

<160> 14

<170> PatentIn version 3.2

<210> 1

<211> 1369

<212> DNA

<213> Homo sapiens

<400> 1

gcacgagaaa ctttgctgtg cgcgttctcc cgcgcgcggg ctcaactttg tagagcgagg 60

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gcggggacac gggtcgcttt gggctcttcc acccctgcgg agcgcactac cccgagccag 180

gggcggtgca agccccgccc ggccctaccc agggcggctc ctccctccgc agcgccgaga 240

cttttagttt cgctttcgct aaaggggccc cagacccttg ctgcggagcg acggagagag 300

actgtgccag tcccagccgc cctaccgccc tgggaacgat ggcagatgat cagggctgta 360

ttgaagagca gggggttgag gattcagcaa atgaagattc agtggatgct aagccagacc 420

ggtcctcggt tgtaccgtcc ctcttcagta agaagaagaa aaatgtcacc atgcgatcca 480

tcaagaccac cggggaccga gtgcctacat atcagtacaa catgaatttt gaaaagctgg 540

gcaaatgcat cataataaac aacaagaact ttgataaagt gacaggtatg ggcgttcgaa 600

acggaacaga caaagatgcc gaggcgctct tcaagtgctt ccgaagcctg ggttttgacg 660

tgattgtcta taatgactgc tcttgtgcca agatgcaaga tctgcttaaa aaagcttctg 720

aagaggacca tacaaatgcc gcctgcttcg cctgcatcct cttagccat ggagaagaaa 780

atgtaattta tgggaaagat ggtgtcacac caataaagga tttgacagcc cactttaggg 840

gggatagatg caaaaccctt ttagagaaac ccaaactctt cttcattcag gcttgccgag 900

ggaccgagct tgatgatgcc atccaggccg actcggggcc catcaatgac acagatgcta 960

atcctcgata caagatccca gtggaagctg acttcctctt cgcctattcc acggttccag 1020  
gctattactc gtggaggagc ccaggaagag gctcctgggt tgtgcaagcc ctctgctcca 1080  
tcctggagga gcacggaaaa gacctggaaa tcatgcagat cctcaccagg gtgaatgaca 1140  
gagttgccag gcactttgag tctcagtctg atgaccaca cttccatgag aagaagcaga 1200  
tcccctgtgt ggtctccatg ctcaccaagg aactctactt cagtcaatag ccatatcagg 1260  
ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc 1320  
ttgaaatatt cagaaattct ccaggatttt aatttcagga aatgtatt 1369

<210> 2  
<211> 303  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser  
1 5 10 15

Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val  
20 25 30

Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile  
35 40 45

Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe  
50 55 60

Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys  
65 70 75 80

Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala  
85 90 95

Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn  
100 105 110

Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu  
115 120 125

Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His  
130 135 140

Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys  
145 150 155 160

Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu  
165 170 175

Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp  
180 185 190

Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn  
195 200 205

Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser  
210 215 220

Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp  
225 230 235 240

Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu  
245 250 255

Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His  
260 265 270

Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile  
275 280 285

Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln  
290 295 300

<210> 3  
<211> 1159  
<212> DNA  
<213> Homo sapiens

<400> 3  
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ctcacacctg tggctgtgta tccgtggcca cagctggttg gcgtcgcctt gaaatcccag 120  
gccgtgagga gtttagcgagc cctgctcaca ctcggcgctc tggttttcgg tgggtgtgcc 180  
ctgcacctgc ctcttcccgc attctcatta ataaaggtat ccatggagaa cactgaaaac 240  
tcagtggatt caaaatccat taaaaatttg gaaccaaaga tcatacatgg aagcgaatca 300  
atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta 360  
tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcgggtctggt 420  
acagatgtcg atgcagcaaa cctcagggaa acattcagaa acttgaaata tgaagtcagg 480

aataaaaaatg atcttacacg tgaagaaatt gtggaattga tgcgtgatgt ttctaaagaa 540  
gatcacagca aaaggagcag ttttgtttgt gtgcttctga gccatggtga agaaggaata 600  
atTTTTggaa caaatggacc tgttgacctg aaaaaataa caaactTTTT cagaggggat 660  
cgTtGtagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca 720  
gaactggact gtggcattga gacagacagt ggtgttgatg atgacatggc gtgtcataaa 780  
ataccagtgg aggccgactt cttgtatgca tactccacag cacctgggta ttattcttgg 840  
cgaaattcaa aggatggctc ctggttcac cagtcgcttt gtgccatgct gaaacagtat 900  
gccgacaagc ttgaatttat gcacattctt acccggtgta accgaaaggt ggcaacagaa 960  
tttgagtctt tttcctttga cgctactttt catgcaaaga aacagattcc atgtattggt 1020  
tccatgctca caaaagaact ctatttttat cactaaagaa atggttggtt ggtggTTTT 1080  
tttagtttgt atgccaagtg agaagatggt atatttgggt actgtatttc cctctcattg 1140  
gggacctact ctcatgctg 1159

<210> 4  
<211> 277  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu  
1 5 10 15

Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser  
20 25 30

Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile  
35 40 45

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg  
50 55 60

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn  
65 70 75 80

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile  
85 90 95

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser  
100 105 110

Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe  
 115 120 125

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg  
 130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile  
 145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser  
 165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp  
 180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn  
 195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys  
 210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
 225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
 245 250 255

His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu  
 260 265 270

Leu Tyr Phe Tyr His  
 275

<210> 5  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Contains a Bam HI restriction enzyme site (underlined) followed  
 by 18 nucleotides of ICE-LAP-3 coding sequence starting from the  
 presumed terminal amino acid of the processed protein codon

<400> 5  
 gatcggatcc atgcgtgcgg ggacacgggt c

31

<210> 6  
 <211> 31

<212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains complementary sequences to an Xba I site followed by 21 nucleotides of ICE-LAP-3  
  
 <400> 6  
 gtactctaga tcattcaccc tgggtggagga t 31  
  
 <210> 7  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains a Bam HI restriction enzyme site followed by 18 nucleotides of ICE-LAP-4 coding sequence starting from the presumed terminal amino acid of the processed protein codon  
  
 <400> 7  
 gatcgatcc atggagaaca ctgaaaactc a 31  
  
 <210> 8  
 <211> 31  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains complementary sequences to an Xba I site followed by 21 nucleotides of ICE-LAP-4  
  
 <400> 8  
 gtactctaga ttagtgataa aaatagagtt c 31  
  
 <210> 9  
 <211> 22  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains the ICE-LAP-3 translational initiation site ATG followed by 5 nucleotides of ICE-LAP-3 coding sequence starting from the initiation codon  
  
 <400> 9  
 gactatgcgt gcggggacac gg 22  
  
 <210> 10  
 <211> 53  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-3 coding sequence, not including the

stop codon

<400> 10  
aatcaagcgt agtctggggac gtcgtatggg tattcacctt ggtggaggat ttg 53

<210> 11  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains the ICE-LAP-4 translational initiation site, ATG,  
followed by 15 nucleotides of ICE-LAP-4 coding sequence starting  
from the initiation codon

<400> 11  
accatggaga acactgaaaa c 21

<210> 12  
<211> 53  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains translation stop codon, HA tag and the last 21  
nucleotides of the ICE-LAP-4 coding sequence, not including the  
stop codon

<400> 12  
aatcaagcgt agtctggggac gtcgtatggg tagtgataaa aatagagttc ttt 53

<210> 13  
<211> 503  
<212> PRT  
<213> Caenorhabditis elegans

<400> 13

Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met  
1 5 10 15

Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala  
20 25 30

Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly  
35 40 45

Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg  
50 55 60

Gly Asp Val Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Ser Thr Gly  
65 70 75 80

His Glu Gly Leu Ala Glu Val Leu Glu Pro Leu Ala Arg Ser Val Asp  
85 90 95

Ser Asn Ala Val Glu Phe Glu Cys Pro Met Ser Pro Ala Ser His Arg  
100 105 110

Arg Ser Arg Ala Leu Ser Pro Ala Gly Tyr Thr Ser Pro Thr Arg Val  
115 120 125

His Arg Asp Ser Val Ser Ser Val Ser Ser Phe Thr Ser Tyr Gln Asp  
130 135 140

Ile Tyr Ser Arg Ala Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser  
145 150 155 160

Ser Asp Arg His Asn Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser  
165 170 175

Gln Pro Ser Ser Ala Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly  
180 185 190

Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr  
195 200 205

Gln Tyr Ile Phe His Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr  
210 215 220

Ile Ser Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser  
225 230 235 240

Pro Arg Gly Met Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met  
245 250 255

Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu  
260 265 270

Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly  
275 280 285

Arg Gly Met Leu Leu Thr Ile Arg Asp Phe Ala Lys His Glu Ser His  
290 295 300

Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Glu Asn Val  
305 310 315 320



Ile Ile Gly Val Asp Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp  
 325 330 335

Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile  
 340 345 350

Val Phe Val Gln Ala Cys Arg Gly Glu Arg Arg Asp Asn Gly Phe Pro  
 355 360 365

Val Leu Asp Ser Val Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp  
 370 375 380

Asp Asn Arg Asp Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro  
 385 390 395 400

Gln Val Gln Gln Val Trp Arg Lys Lys Pro Ser Gln Ala Asp Ile Leu  
 405 410 415

Ile Ala Tyr Ala Thr Thr Ala Gln Tyr Val Ser Trp Arg Asn Ser Ala  
 420 425 430

Arg Gly Ser Trp Phe Ile Gln Ala Val Cys Glu Val Phe Ser Thr His  
 435 440 445

Ala Lys Asp Met Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys  
 450 455 460

Val Ala Cys Gly Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln  
 465 470 475 480

Met Pro Glu Met Thr Ser Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro  
 485 490 495

Glu Ala Arg Asn Ser Ala Val  
 500

<210> 14  
 <211> 404  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser  
 1 5 10 15

Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr  
 20 25 30  
 Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala  
 35 40 45  
 Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys  
 50 55 60  
 Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp  
 65 70 75 80  
 Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly  
 85 90 95  
 Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro  
 100 105 110  
 Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly  
 115 120 125  
 Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile  
 130 135 140  
 Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser  
 145 150 155 160  
 Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile  
 165 170 175  
 Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu  
 180 185 190  
 Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala  
 195 200 205  
 Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His  
 210 215 220  
 Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg  
 225 230 235 240  
 Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu  
 245 250 255

Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser  
260 265 270

Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Asp  
275 280 285

Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn  
290 295 300

Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys  
305 310 315 320

Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp  
325 330 335

Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg  
340 345 350

Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu  
355 360 365

Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala  
370 375 380

Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu  
385 390 395 400

Phe Pro Gly His